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<150> JP 2003-379114

<151> 2003. 11. 7

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<170> PatentIn Ver. 3.1

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 Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala
 630 635 640

aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac
 Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn
 645 650 655

ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa
 Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu
 660 665 670

tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa
 Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
 675 680 685

att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt
 Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
 690 695 700 705

aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga
 Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
 710 715 720

gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg
 Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
 725 730 735

gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat
 Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
 740 745 750

gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa
 Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
 755 760 765

gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca
 Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
 770 775 780 785

atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct

2283

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3003

3051

3105

aaaggctcga tgcagatctt ttagataacc ttttttgcga taactggaca tagaatggtt 3165
attaaagaaa gcaagggtgt tttacgatat taaaaaggta gcgatittaa attgaaacct 3225
ttaataatgt ctltgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac 3285
ggaaatttct agtagaagaa aaacagacca agaaatactg caagctt 3332

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<212> PRT
<213> Bacillus sp. KSM-64

<400> 4

Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile
-25 -20 -15

Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala Glu Gly
-10 -5 -1 1

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
5 10 15

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
20 25 30 35

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
40 45 50

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
55 60 65

Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile Arg Leu
70 75 80

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu Leu Ile
85 90 95

Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn Asp Met
100 105 110 115

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
120 125 130

Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala Ala Leu
135 140 145

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
150 155 160

Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
165 170 175

Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Asp
180 185 190 195

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
 200 205 210
 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
 215 220 225
 Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
 230 235 240
 Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
 245 250 255
 Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
 260 265 270 275
 Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr Phe Asp
 280 285 290
 Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
 295 300 305
 Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
 310 315 320
 Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro Gly Pro
 325 330 335
 Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
 340 345 350 355
 Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
 360 365 370
 Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
 375 380 385
 Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu Asn Glu
 390 395 400
 Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp Val Ser
 405 410 415
 Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly Trp Gly
 420 425 430 435
 Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val Ile
 440 445 450
 Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln Gly Pro
 455 460 465
 Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu Pro Thr
 470 475 480

Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr Ile Thr
 485 490 495

Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala Glu Asn
 500 505 510 515

Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly Ala Asp
 520 525 530

Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile
 535 540 545

Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe
 550 555 560

Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val
 565 570 575

Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser
 580 585 590 595

Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr
 600 605 610

Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn
 615 620 625

Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu
 630 635 640

Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr
 645 650 655

Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu
 660 665 670 675

Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn
 680 685 690

Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met
 695 700 705

Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe
 710 715 720

Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu
 725 730 735

Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys
 740 745 750 755

Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala
 760 765 770

Asn Glu Ala Thr Lys Lys
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<400> 6
ctaattgggtg cttagttgc tgataccgac gataatgcc 39

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<211> 37
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<400> 7
ctgccccgtt agttgaagag actgccctcc ttttcgg 37

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cgcaaactca taaaaatcat attt 24

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<400> 9
caactaaagc acccattagt tcaaca 26

<210> 10
<211> 27
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<400> 10
cttcaactaa cggggcaggt tagtgac 27

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<400> 11
cagatgalat ggtgaaaaaa tcaatccg 29

<210> 12
<211> 38

<212> **WO 2005/045045**
<213> Artificial Sequence

PCT/JP2004/016890

<400> 12
gttatccgct cacaattccg agctgcata cagatccc 38

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<400> 13
cgtcgtgact gggaaaactg ttgattacaa agaggcag 38

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<400> 14
ccatcggcca aatataagac acagccaacg c 31

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<400> 15
gaattgtgag cggataac 18

<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence

<400> 16
gttttcccag tcacgacg 18

<210> 17
<211> 20
<212> DNA
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<400> 17
ataatgcccg cttcccaacc 20

<210> 18
<211> 38
<212> DNA
<213> Artificial Sequence

<400> 18
gttatccgct cacaattccg atcctcagct cctttgtc 38

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<400> 19
cgtcgtgact gggaaaactc atcigatacc gattaacc 38

<210> 20
<211> 20
<212> DNA

<400> 20
caactgaatc cgaaggaatg 20

<210> 21
<211> 2343
<212> DNA
<213> Bacillus sp. pHSP-K38

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<222> (580).. (627)
<223>

<220>
<221> mat_peptide
<222> (628).. 0
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tgaatcacgga ataaaatcag gtaaacagggt cctgatttta tttttttgaa tttttttgag 120
aactaaagat tgaatatagaa gtagaagaca acggacataa gaaaattgta itagttttta 180
ttatagaaaa cgctttttcta taattattta tacctagaac gaaaatactg tttcgaaagc 240
ggtttactat aaaaccttat attccggctc tttttttaaa caggggggtga aaattcactc 300
tagtatctta atttcaacat gctataataa atttgtaaga cgcaatatac atcttttttt 360
tatgatattt gtaagcgggt aaccttgtgc tatatgccga tttaggaagg gggtagattg 420
agtcaagtag tcataattta gataacttat aagtigtgtga gaagcaggag agaattctggg 480
ttactcaciaa gttttttaaa acattatcga aagcactttc ggttatgctt atgaatttag 540
ctatttgatt caattacttt aataatttta ggaggtaat atg atg tta aga aag 594
Met Met Leu Arg Lys
-15
aaa aca aag cag ttg ggt cga cca gca caa gcc gat gga ttg aac ggt 642
Lys Thr Lys Gln Leu Gly Arg Pro Ala Gln Ala Asp Gly Leu Asn Gly
-10 -5 -1 1 5
acg atg atg cag tat tat gag tgg cat ttg gaa aac gac ggg cag cat 690
Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp Gly Gln His
10 15 20
tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat gct ggt att 738
Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp Ala Gly Ile
25 30 35
aca gct att tgg att ccg cca gcc tac aaa ggt aat agt cag gcg gat 786
Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp
40 45 50
gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag ttc aat caa 834
Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln
55 60 65
aag ggt act gtt cga acg aaa tac gga act aag gca cag ctt gaa cga 882
Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg
70 75 80 85

WO 2005/045045
gct att ggt tcc ctt caa tct aat gat atc aat gta tac gga gat gtc 930 PCT/JP2004/016890
Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr Gly Asp Val
90 95 100

gtg atg aat cat aaa atg gga gct gat ttt acg gag gca gtg caa gct 978
Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala Val Gln Ala
105 110 115

gtt caa gta aat cca acg aat cgt tgg cag gat att tca ggt gcc tac 1026
Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser Gly Ala Tyr
120 125 130

acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt aac aac gcc 1074
Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala
135 140 145

tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt gtt gac tgg 1122
Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly Val Asp Trp
150 155 160 165

gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca aat acg aac 1170
Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala Asn Thr Asn
170 175 180

tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat tac ctg tta 1218
Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu
185 190 195

gga tcg aat atc gac ttt agt cat cca gaa gta caa gat gag ttg aag 1266
Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp Glu Leu Lys
200 205 210

gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat ggt tat cgt 1314
Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg
215 220 225

tta gat gct att aaa cat att cca ttc tgg tat aca tct gat tgg gtt 1362
Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val
230 235 240 245

cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc gta ggg gaa 1410
Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val Val Gly Glu
250 255 260

tat tgg aag gat gac gta ggt gct ctc gaa ttt tat tta gat gaa atg 1458
Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met
265 270 275

aat tgg gag atg tct cta ttc gat gtt cca ctt aat tat aat ttt tac 1506
Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr
280 285 290

cgg gct tca caa caa ggt gga agc tat gat atg cgt aat att tta cga 1554
Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg
295 300 305

gga tct tta gta gaa gcg cat ccg atg cat gca gtt acg ttt gtt gat 1602
Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr Phe Val Asp
310 315 320 325

aat cat gat act cag cca ggg gag tca tta gag tca tgg gtt gct gat 1650
Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp Val Ala Asp
330 335 340

tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt gaa ggt ggt 1698
Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly
345 350 355

tat cca aat gta ttt tac ggt gat tac tat ggg att cct aac gat aac 1746
Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn
360 365 370

att tca gct aaa aaa gat atg att gat gag ctg ctt gat gca cgt caa 1794

Ile Ser Met Ile Asp Glu Leu Leu Asp Ala Arg Gln
 375 380 385

PCT/JP2004/016890

aat tac gca tat ggc acg cag cat gac tat ttt gat cat tgg gat gtt 1842
 Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His Trp Asp Val
 390 395 400 405

gta gga tgg act agg gaa gga tct tcc tcc aga cct aat tca ggc ctt 1890
 Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu
 410 415 420

gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg atg tat gta 1938
 Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp Met Tyr Val
 425 430 435

gga cgt cag aat gca gga caa aca tgg aca gat tta act ggt aat aac 1986
 Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn
 440 445 450

gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa ttc ttt acg 2034
 Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr
 455 460 465

aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaag ccttgagaag 2087
 Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 470 475 480

ggattccccc ctaactcaag gctttcttta tgcgccttag ctttacgctt ctacgacttt 2147

gaagcttggg gatccgtcga gacaaggtaa aggataaaac agcacaattc caagaaaaac 2207

acgatttaga acctaaaaag aacgaatttg aactaactca taaccgagag gtaaaaaaag 2267

aacgaagtcg agatcaggga atgagtttat aaaataaaaa aagcacctga aaagggtgtct 2327

ttttttgatg tctaga 2343

<210> 22
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 <213> Bacillus sp. pHSP-K38

<400> 22

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Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
 1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
 20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Thr Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

PCT/JP2004/016890

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe

385 WO 2005/045045 90

395

400

PCT/JP2004/016890

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480